RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _08/444,791B_

Source: _1Fw/6_

Date Processed by STIC: _10/17/05_

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RAW SEQUENCE LISTING　　　　　　　　　　DATE: 10/17/2005
PATENT APPLICATION:　US/08/444,791B　　　TIME: 12:31:09

Input Set : **A:\40451c.txt**
Output Set: **N:\CRF4\10172005\H444791B.raw**

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 3 <110> APPLICANT: Brockhaus, et al.
 5 <120> TITLE OF INVENTION: Human TNF Receptor
 7 <130> FILE REFERENCE: 01017/40451C
 9 <140> CURRENT APPLICATION NUMBER: US 08/444,791B
10 <141> CURRENT FILING DATE: 1995-05-19
12 <150> PRIOR APPLICATION NUMBER: US 08/095,640
13 <151> PRIOR FILING DATE: 1993-07-21
15 <150> PRIOR APPLICATION NUMBER: US 07/580,013
16 <151> PRIOR FILING DATE: 1990-09-10
18 <150> PRIOR APPLICATION NUMBER: CH 1347/90
19 <151> PRIOR FILING DATE: 1990-04-20
21 <150> PRIOR APPLICATION NUMBER: CH 746/90
22 <151> PRIOR FILING DATE: 1990-03-08  ·
24 <150> PRIOR APPLICATION NUMBER: CH 3319/89
25 <151> PRIOR FILING DATE: 1989-09-12
27 <160> NUMBER OF SEQ ID NOS: 26
29 <170> SOFTWARE: PatentIn version 3.3
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 2111
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
36 <400> SEQUENCE: 1
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39 ccctcaactg tcaccccaag gcacttggga cgtcctggac agaccgagtc ccgggaagcc   120
41 ccagcactgc cgctgccaca ctgccctgag cccaaatggg ggagtgagag gccatagctg   180
43 tctggcatgg gcctctccac cgtgcctgac ctgctgctgc cgctggtgct cctggagctg   240
45 ttggtgggaa tatacccctc aggggttatt ggactggtcc ctcacctagg gacagggag   300
47 aagagagata gtgtgtgtcc ccaaggaaaa tatatccacc ctcaaaataa ttcgatttgc   360
49 tgtaccaagt gccacaaagg aacctacttg tacaatgact gtccaggccc ggggcaggat   420
51 acggactgca gggagtgtga gagcggctcc ttcaccgctt cagaaaacca cctcagacac   480
53 tgcctcagct gctccaaatg ccgaaaggaa atgggtcagg tggagatctc ttcttgcaca   540
55 gtggaccggg acaccgtgtg tggctgcagg aagaaccagt accggcatta ttggagtgaa   600
57 aacctttttcc agtgcttcaa ttgcagcctc tgcctcaatg gaccgtgca cctctcctgc   660
59 caggagaaac agaacaccgt gtgcacctgc catgcaggtt tctttctaag agaaaacgag   720
61 tgtgtctcct gtagtaactg taagaaaagc ctggagtgca cgaagttgtg cctaccccag   780
63 attgagaatg ttaagggcac tgaggactca ggcaccacag tgctgttgcc cctggtcatt   840
65 ttctttggtc tttgcctttt atccctcctc ttcattggtt taatgtatcg ctaccaacgg   900
67 tggaagtcca agctctactc cattgtttgt gggaaatcga cacctgaaaa agagggggag  960
69 cttgaaggaa ctactactaa gccctggcc ccaaacccaa gcttcagtcc cactccaggc  1020
71 ttcaccccca ccctgggctt cagtcccgtg cccagttcca ccttcacctc cagctccacc  1080
73 tatacccccg gtgactgtcc caactttgcg gctccccgca gagaggtggc accaccctat  1140
75 caggggggctg accccatcct tgcgacagcc ctcgcctccg accccatccc caaccccctt  1200
77 cagaagtggg aggacagcgc ccacaagcca cagagcctag acactgatga ccccgcgacg  1260
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 79 ctgtacgccg tggtggagaa cgtgcccccg ttgcgctgga aggaattcgt gcggcgccta  1320
 81 gggctgagcg accacgagat cgatcggctg gagctgcaga acgggcgctg cctgcgcgag  1380
 83 gcgcaataca gcatgctggc gacctggagg cggcgcacgc cgcggcgcga ggccacgctg  1440
 85 gagctgctgg gacgcgtgct ccgcgacatg gacctgctgg gctgcctgga ggacatcgag  1500
 87 gaggcgcttt gcggccccgc cgccctcccg cccgcgccca gtcttctcag atgaggctgc  1560
 89 gcccctgcgg gcagctctaa ggaccgtcct gcgagatcgc cttccaaccc cacttttttc  1620
 91 tggaaaggag gggtcctgca ggggcaagca ggagctagca gccgcctact tggtgctaac  1680
 93 ccctcgatgt acatagcttt tctcagctgc ctgcgcgccg ccgacagtca gcgctgtgcg  1740
 95 cgcggagaga ggtgcgccgt gggctcaaga gcctgagtgg gtggtttgcg aggatgaggg  1800
 97 acgctatgcc tcatgcccgt tttgggtgtc ctcaccagca aggctgctcg ggggcccctg  1860
 99 gttcgtccct gagccttttt cacagtgcat aagcagtttt ttttgttttt gttttgtttt  1920
101 gttttgtttt taaatcaatc atgttacact aatagaaact tggcactcct gtgccctctg  1980
103 cctggacaag cacatagcaa gctgaactgt cctaaggcag gggcgagcac ggaacaatgg  2040
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107 aacccgaatt c                                                       2111
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110 <210> SEQ ID NO: 2
111 <211> LENGTH: 455
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 2

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121 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
122             20                  25                  30
125 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
126         35                  40                  45
129 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
130     50                  55                  60
133 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
134 65                  70                  75                  80
137 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
138             85                  90                  95
141 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
142             100                 105                 110
145 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
146         115                 120                 125
149 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
150     130                 135                 140
153 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
154 145                 150                 155                 160
157 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
158             165                 170                 175
161 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
162             180                 185                 190
165 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
166         195                 200                 205
169 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
170     210                 215                 220
173 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
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174 225                   230                 235                    240
177 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
178                   245                 250                    255
181 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
182             260                 265                270
185 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
186         275                 280                 285
189 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
190     290                 295                300
193 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
194 305                   310                 315                    320
197 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
198             325                 330                    335
201 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
202             340                 345                350
205 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
206         355                 360                 365
209 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
210     370                 375                380
213 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
214 385                   390                 395                    400
217 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
218             405                 410                    415
221 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
222             420                 425                430
225 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
226         435                 440                 445
229 Pro Ala Pro Ser Leu Leu Arg
230     450                 455
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233 <210> SEQ ID NO: 3
234 <211> LENGTH: 2339
235 <212> TYPE: DNA
236 <213> ORGANISM: Homo sapiens
238 <400> SEQUENCE: 3

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241 cccgagtgct tgagctgtgg ctcccgctgt agctctgacc aggtggaaac tcaagcctgc   120
243 actcgggaac agaaccgcat ctgcacctgc aggcccggct ggtactgcgc gctgagcaag   180
245 caggaggggt gccggctgtg cgcgccgctg ccgaagtgcc gcccgggctt cggcgtggcc   240
247 agaccaggaa ctgaaacatc agacgtggtg tgcaagccct gtgccccggg gacgttctcc   300
249 aacacgactt catccacgga tatttgcagg ccccaccaga tctgtaacgt ggtggccatc   360
251 cctgggaatg caagcaggga tgcagtctgc acgtccacgt cccccacccg gagtatggcc   420
253 ccaggggcag tacacttacc ccagccagtg tccacacgat cccaacacac gcagccaagt   480
255 ccagaaccca gcactgctcc aagcacctcc ttcctgctcc caatgggccc cagcccccca   540
257 gctgaaggga gcactggcga cttcgctctt ccagttggac tgattgtggg tgtgacagcc   600
259 ttgggtctac taataatagg agtggtgaac tgtgtcatca tgacccaggt gaaaaagaag   660
261 cccttgtgcc tgcagagaga agccaaggtg cctcacttgc ctgccgataa ggcccggggt   720
263 acacagggcc ccgagcagca gcacctgctg atcacagcgc cgagctccag cagcagctcc   780
265 ctggagagct cggccagtgc gttggacaga agggcgccca ctcggaacca gccacaggca   840
267 ccaggcgtgg aggccagtgg ggccggggag gcccgggcca gcaccgggag ctcagcagat   900
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269 tcttcccctg gtggccatgg gacccaggtc aatgtcacct gcatcgtgaa cgtctgtagc      960
271 agctctgacc acagctcaca gtgctcctcc caagccagct ccacaatggg agacacagat     1020
273 tccagcccct cggagtcccc gaaggacgag caggtcccct tctccaagga ggaatgtgcc     1080
275 tttcggtcac agctggagac gccagagacc ctgctgggga gcaccgaaga gaagcccctg     1140
277 cccccttggag tgcctgatgc tgggatgaag cccagttaac caggccggtg tgggctgtgt     1200
279 cgtagccaag gtggctgagc cctggcagga tgaccctgcg aaggggccct ggtccttcca     1260
281 ggcccccacc actaggactc tgaggctctt tctgggccaa gttcctctag tgccctccac     1320
283 agccgcagcc tccctctgac ctgcaggcca agagcagagg cagcgagttg tggaaagcct     1380
285 ctgctgccat ggcgtgtccc tctcggaagg ctggctgggc atggacgttc ggggcatgct     1440
287 ggggcaagtc cctgagtctc tgtgacctgc cccgcccagc tgcacctgcc agcctggctt     1500
289 ctggagccct tgggtttttt gtttgtttgt ttgtttgttt gtttgtttct cccctgggc     1560
291 tctgcccagc tctggcttcc agaaaacccc agcatccttt tctgcagagg ggctttctgg     1620
293 agaggaggga tgctgcctga gtcacccatg aagacaggac agtgcttcag cctgaggctg     1680
295 agactgcggg atggtcctgg ggctctgtgc agggaggagg tggcagccct gtagggaacg     1740
297 gggtccttca agttagctca ggaggcttgg aaagcatcac ctcaggccag gtgcagtggc     1800
299 tcacgcctat gatcccagca ctttgggagg ctgaggcggg tggatcacct gaggttagga     1860
301 gttcgagacc agcctggcca acatggtaaa accccatctc tactaaaaat acagaaatta     1920
303 gccgggcgtg gtggcgggca cctatagtcc cagctactca gaagcctgag gctgggaaat     1980
305 cgtttgaacc cgggaagcgg aggttgcagg gagccgagat cacgccactg cactccagcc     2040
307 tgggcgacag agcgagagtc tgtctcaaaa gaaaaaaaaa aagcaccgcc tccaaatgct     2100
309 aacttgtcct tttgtaccat ggtgtgaaag tcagatgccc agagggccca ggcaggccac     2160
311 catattcagt gctgtggcct gggcaagata cgcacttct aactagaaat ctgccaattt     2220
313 tttaaaaaag taagtaccac tcaggccaac aagccaacga caaagccaaa ctctgccagc     2280
315 cacatccaac cccccacctg ccatttgcac cctccgcctt cactccggtg tgcctgcag     2339
318 <210> SEQ ID NO: 4
319 <211> LENGTH: 392
320 <212> TYPE: PRT
321 <213> ORGANISM: Homo sapiens
323 <400> SEQUENCE: 4
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326 1               5                   10                  15
329 Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
330             20                  25                  30
333 Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
334         35                  40                  45
337 Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
338     50                  55                  60
341 Arg Leu Cys Ala Pro Leu Pro Lys Cys Arg Pro Gly Phe Gly Val Ala
342 65                  70                  75                  80
345 Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
346             85                  90                  95
349 Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
350             100                 105                 110
353 Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala
354         115                 120                 125
357 Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
358     130                 135                 140
361 His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Ser
362 145                 150                 155                 160
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365 Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
366             165             170             175
369 Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val
370             180             185             190
373 Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val
374         195             200             205
377 Val Asn Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu
378         210             215             220
381 Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly
382 225             230             235             240
385 Thr Gln Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser
386             245             250             255
389 Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala
390             260             265             270
393 Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala
394         275             280             285
397 Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Ala Asp Ser Ser Pro Gly
398         290             295             300
401 Gly His Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser
402 305             310             315             320
405 Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met
406             325             330             335
409 Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val
410             340             345             350
413 Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro
414         355             360             365
417 Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val
418         370             375             380
421 Pro Asp Ala Gly Met Lys Pro Ser
422 385             390
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426 <211> LENGTH: 28
427 <212> TYPE: PRT
428 <213> ORGANISM: Artificial sequence
430 <220> FEATURE:
431 <223> OTHER INFORMATION: Synthetic peptide
434 <220> FEATURE:
435 <221> NAME/KEY: misc_feature
436 <222> LOCATION: (25)..(25)
437 <223> OTHER INFORMATION: Xaa = unknown amino acid
439 <400> SEQUENCE: 5
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446             20              25
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449 <211> LENGTH: 15
450 <212> TYPE: PRT
451 <213> ORGANISM: Artificial sequence
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/17/2005
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 25
Seq#:10; Xaa Pos. 8
Seq#:11; Xaa Pos. 2
Seq#:14; Xaa Pos. 9,10,13

VERIFICATION SUMMARY   DATE: 10/17/2005
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L:445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:16
L:524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:601 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0